



SEQUENCE LISTING

<110> Fischer, Robert L.
Mizukami, Yukiko
The Regents of the University of California

<120> Methods for Altering Organ Mass, Controlling Fertility
and Enhancing Asexual Reproduction in Plants

<130> 023070-090720US

<140> US 09/479,855
<141> 2000-01-07

<160> 8

<170> PatentIn Ver. 2.1

<210> 1
<211> 2148
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> AINTEGUMENTA (ANT) cDNA

<220>
<221> CDS
<222> (269)..(1936)
<223> AINTEGUMENTA (ANT)

<400> 1
agatccaaac ggattcaaacc agcaaatttg tgctttgctc ttctctctta ttataatatac 60
ctctcaaaaa ccctctccta tatttcctta aagccccct tccttgcgtc tctaccgcaa 120
caaagaaaaa acaaaagttt gagaaaaatg gtgtgttcgt tgtgttaacca atgattgggt 180
tttagttac tacttcgaga gattataaga aagaaagagt gaagatacat tatagaaaaga 240
agagaagcag aaacaaaaaa aagaaacc atg aag tct ttt tgt gat aat gat 292
Met Lys Ser Phe Cys Asp Asn Asp
1 5

gat aat aat cat agc aac acg act aat ttg tta ggg ttc tca ttg tct 340
Asp Asn Asn His Ser Asn Thr Thr Asn Leu Leu Gly Phe Ser Leu Ser
10 15 20

tca aat atg atg aaa atg gga ggt aga gga ggt aga gaa gct att tac 388
Ser Asn Met Met Lys Met Gly Gly Arg Gly Arg Glu Ala Ile Tyr
25 30 35 40

tca tct tca act tct tca gct gca act tct tct tct gtt cca cct 436
Ser Ser Ser Thr Ser Ser Ala Ala Thr Ser Ser Ser Val Pro Pro
45 50 55

caa ctt gtt gtt ggt gac aac act agc aac ttt ggt gtt tgc tat gga 484
Gln Leu Val Val Gly Asp Asn Thr Ser Asn Phe Gly Val Cys Tyr Gly
60 65 70

tct aac cca aat gga gga atc tat tct cac atg tct gtg atg cca ctc Ser Asn Pro Asn Gly Gly Ile Tyr Ser His Met Ser Val Met Pro Leu	75 80 85	532
aga tct gat ggt tct ctt tgc tta atg gaa gct ctc aac aga tct tct Arg Ser Asp Gly Ser Leu Cys Leu Met Glu Ala Leu Asn Arg Ser Ser	90 95 100	580
cac tcg aat cac cat caa gat tca tct cca aag gtg gag gat ttc ttt His Ser Asn His His Gln Asp Ser Ser Pro Lys Val Glu Asp Phe Phe	105 110 115	628
ggg acc cat cac aac aac aca agt cac aaa gaa gcc atg gat ctt agc Gly Thr His His Asn Asn Thr Ser His Lys Glu Ala Met Asp Leu Ser	125 130 135	676
tta gat agt tta ttc tac aac acc act cat gag ccc aac acg act aca Leu Asp Ser Leu Phe Tyr Asn Thr Thr His Glu Pro Asn Thr Thr Thr	140 145 150	724
aac ttt caa gag ttc ttt agc ttc cct caa acc aga aac cat gag gaa Asn Phe Gln Glu Phe Phe Ser Phe Pro Gln Thr Arg Asn His Glu Glu	155 160 165	772
gaa act aga aat tac ggg aat gac cct agt ttg aca cat gga ggg tct Glu Thr Arg Asn Tyr Gly Asn Asp Pro Ser Leu Thr His Gly Gly Ser	170 175 180	820
ttt aat gta ggg gta tat ggg gaa ttt caa cag tca ctg agc tta tcc Phe Asn Val Gly Val Tyr Gly Glu Phe Gln Gln Ser Leu Ser Leu Ser	185 190 195	868
atg agc cct ggg tca caa tct agc tgc atc act ggc tct cac cac cac Met Ser Pro Gly Ser Gln Ser Ser Cys Ile Thr Gly Ser His His His	205 210 215	916
caa caa aac caa aac caa aac cac caa agc caa aac cac cag cag atc Gln Gln Asn Gln Asn His Gln Ser Gln Asn His Gln Gln Ile	220 225 230	964
tct gaa gct ctt gtg gag aca agc gtt ggg ttt gag acg acg aca atg Ser Glu Ala Leu Val Glu Thr Ser Val Gly Phe Glu Thr Thr Thr Met	235 240 245	1012
gcg gct gcg aag aag aag agg gga caa gag gat gtt gta gtt gtt ggt Ala Ala Ala Lys Lys Lys Arg Gly Gln Glu Asp Val Val Val Val Gly	250 255 260	1060
cag aaa cag att gtt cat aga aaa tct atc gat act ttt gga caa cga Gln Lys Gln Ile Val His Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg	265 270 275	1108
act tct caa tac cga ggc gtt aca aga cat aga tgg act ggt aga tat Thr Ser Gln Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr	285 290 295	1156
gaa gct cat cta tgg gac aat agt ttc aag aag gaa ggt cac agt aga Glu Ala His Leu Trp Asp Asn Ser Phe Lys Lys Glu Gly His Ser Arg	300 305 310	1204

aaa gga aga caa gtt tat ctg gga ggt tat gat atg gag gag aaa gct Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Met Glu Glu Lys Ala 315 320 325	1252
gct cga gca tat gat ctt gct gca ctc aag tac ttg ggt ccc tct act Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Ser Thr 330 335 340	1300
cac acc aat ttc tct gcg gag aat tat cag aaa gag att gaa gac atg His Thr Asn Phe Ser Ala Glu Asn Tyr Gln Lys Glu Ile Glu Asp Met 345 350 355 360	1348
aag aac atg act aga caa gaa tat gtt gca cat ttg aga agg aag agc Lys Asn Met Thr Arg Gln Glu Tyr Val Ala His Leu Arg Arg Lys Ser 365 370 375	1396
agt ggt ttc tct agg ggt gct tcc atc tat aga gga gtc aca aga cat Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His 380 385 390	1444
cac cag cat gga agg tgg caa gca cg att ggt aga gtc gct gga aac His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn 395 400 405	1492
aaa gat ctc tac ctt gga act ttt gga acc caa gaa gaa gct gca gaa Lys Asp Leu Tyr Leu Gly Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu 410 415 420	1540
gct tac gat gta gca gca att aag ttc cgt ggc aca aat gct gtg act Ala Tyr Asp Val Ala Ala Ile Lys Phe Arg Gly Thr Asn Ala Val Thr 425 430 435 440	1588
aac ttt gat atc acg agg tac gat gtt gat cgt atc atg tct agt aac Asn Phe Asp Ile Thr Arg Tyr Asp Val Asp Arg Ile Met Ser Ser Asn 445 450 455	1636
aca ctc ttg tct gga gag tta gcg cga agg aac aac aac agc att gtc Thr Leu Leu Ser Gly Glu Leu Ala Arg Arg Asn Asn Ser Ile Val 460 465 470	1684
gtc agg aat act gaa gac caa acc gct cta aat gct gtt gtg gaa ggt Val Arg Asn Thr Glu Asp Gln Thr Ala Leu Asn Ala Val Val Glu Gly 475 480 485	1732
ggt tcc aac aaa gaa gtc agt act ccc gag aga ctc ttg agt ttt ccg Gly Ser Asn Lys Glu Val Ser Thr Pro Glu Arg Leu Leu Ser Phe Pro 490 495 500	1780
gcg att ttc gcg ttg cct caa gtt aat caa aag atg ttc gga tca aat Ala Ile Phe Ala Leu Pro Gln Val Asn Gln Lys Met Phe Gly Ser Asn 505 510 515 520	1828
atg ggc gga aat atg agt cct tgg aca tca aac cct aat gct gag ctt Met Gly Asn Met Ser Pro Trp Thr Ser Asn Pro Asn Ala Glu Leu 525 530 535	1876
aag acc gtc gct ctt act ttg cct cag atg ccg gtt ttc gct gct tgg Lys Thr Val Ala Leu Thr Leu Pro Gln Met Pro Val Phe Ala Ala Trp 540 545 550	1924

gct gat tct tga tcaacttcaa tgactaactc tggtttctt ggtttagttg 1976
 Ala Asp Ser
 555

ctaagtgttt tggtttatct ccggtttat ccggtttgaa ctacaattcg gttagtttc 2036
 gtcggataaa atagtatttgc cttaggagcg gtatatgtt ctttgagta gtattcatgt 2096
 gaaacagaat gaatctctct ataacatatt atttaatga atctcccttg ct 2148

<210> 2
 <211> 555
 <212> PRT
 <213> *Arabidopsis thaliana*
 <223> AINTEGUMENTA (ANT)

<400> 2
 Met Lys Ser Phe Cys Asp Asn Asp Asn Asn His Ser Asn Thr Thr
 1 5 10 15
 Asn Leu Leu Gly Phe Ser Leu Ser Ser Asn Met Met Lys Met Gly Gly
 20 25 30
 Arg Gly Arg Glu Ala Ile Tyr Ser Ser Ser Thr Ser Ser Ala Ala
 35 40 45
 Thr Ser Ser Ser Val Pro Pro Gln Leu Val Val Gly Asp Asn Thr
 50 55 60
 Ser Asn Phe Gly Val Cys Tyr Gly Ser Asn Pro Asn Gly Gly Ile Tyr
 65 70 75 80
 Ser His Met Ser Val Met Pro Leu Arg Ser Asp Gly Ser Leu Cys Leu
 85 90 95
 Met Glu Ala Leu Asn Arg Ser Ser His Ser Asn His His Gln Asp Ser
 100 105 110
 Ser Pro Lys Val Glu Asp Phe Phe Gly Thr His His Asn Asn Thr Ser
 115 120 125
 His Lys Glu Ala Met Asp Leu Ser Leu Asp Ser Leu Phe Tyr Asn Thr
 130 135 140
 Thr His Glu Pro Asn Thr Thr Asn Phe Gln Glu Phe Phe Ser Phe
 145 150 155 160
 Pro Gln Thr Arg Asn His Glu Glu Glu Thr Arg Asn Tyr Gly Asn Asp
 165 170 175
 Pro Ser Leu Thr His Gly Gly Ser Phe Asn Val Gly Val Tyr Gly Glu
 180 185 190
 Phe Gln Gln Ser Leu Ser Leu Ser Met Ser Pro Gly Ser Gln Ser Ser
 195 200 205
 Cys Ile Thr Gly Ser His His His Gln Gln Asn Gln Asn Gln Asn His
 210 215 220
 Gln Ser Gln Asn His Gln Gln Ile Ser Glu Ala Leu Val Glu Thr Ser
 225 230 235 240
 Val Gly Phe Glu Thr Thr Met Ala Ala Ala Lys Lys Lys Arg Gly
 245 250 255
 Gln Glu Asp Val Val Val Gly Gln Lys Gln Ile Val His Arg Lys
 260 265 270
 Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Gln Tyr Arg Gly Val Thr
 275 280 285
 Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser
 290 295 300
 Phe Lys Lys Glu Gly His Ser Arg Lys Gly Arg Gln Val Tyr Leu Gly
 305 310 315 320
 Gly Tyr Asp Met Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala
 325 330 335

Leu	Lys	Tyr	Trp	Gly	Pro	Ser	Thr	His	Thr	Asn	Phe	Ser	Ala	Glu	Asn
340					345								350		
Tyr	Gln	Lys	Glu	Ile	Glu	Asp	Met	Lys	Asn	Met	Thr	Arg	Gln	Glu	Tyr
355					360							365			
Val	Ala	His	Leu	Arg	Arg	Lys	Ser	Ser	Gly	Phe	Ser	Arg	Gly	Ala	Ser
370					375							380			
Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	His	Gln	His	Gly	Arg	Trp	Gln	Ala
385					390					395				400	
Arg	Ile	Gly	Arg	Val	Ala	Gly	Asn	Lys	Asp	Leu	Tyr	Leu	Gly	Thr	Phe
							405			410				415	
Gly	Thr	Gln	Glu	Glu	Ala	Ala	Glu	Ala	Tyr	Asp	Val	Ala	Ala	Ile	Lys
							420			425				430	
Phe	Arg	Gly	Thr	Asn	Ala	Val	Thr	Asn	Phe	Asp	Ile	Thr	Arg	Tyr	Asp
							435			440				445	
Val	Asp	Arg	Ile	Met	Ser	Ser	Asn	Thr	Leu	Leu	Ser	Gly	Glu	Leu	Ala
							450			455				460	
Arg	Arg	Asn	Asn	Asn	Ser	Ile	Val	Val	Arg	Asn	Thr	Glu	Asp	Gln	Thr
							465			470				475	
Ala	Leu	Asn	Ala	Val	Val	Glu	Gly	Gly	Ser	Asn	Lys	Glu	Val	Ser	Thr
							485			490				495	
Pro	Glu	Arg	Leu	Leu	Ser	Phe	Pro	Ala	Ile	Phe	Ala	Leu	Pro	Gln	Val
							500			505				510	
Asn	Gln	Lys	Met	Phe	Gly	Ser	Asn	Met	Gly	Gly	Asn	Met	Ser	Pro	Trp
							515			520				525	
Thr	Ser	Asn	Pro	Asn	Ala	Glu	Leu	Lys	Thr	Val	Ala	Leu	Thr	Leu	Pro
							530			535				540	
Gln	Met	Pro	Val	Phe	Ala	Ala	Trp	Ala	Asp	Ser					
							545			550				555	

<210> 3
<211> 4228
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> ANT gene 5' promoter

<400> 3
gtcgactcta ggcctcaactg gcctaatacg actcactata gggagctcga ggatccttta 60
gttagaaaaa actttctttg tacgtgtgtg tgggtgtttt aagtccattt ataaactatgc 120
acatgtata tcacaatata tatattgtaaa ttgaaattat tcatattaat gagtttagcat 180
taatatataat acgctgacat taccaaccaa atgtttctgc ttgttatggat agttctatata 240
gttcacttg attatagata ctatataaaa ctgggtttat ttaaaatccg tacccataac 300
aaaagtggac caaaaacgaga tccatgggtt tgggtttact ttgttggta accagataat 360
atgattatgg aagatttaat ctttactaaa ttataaaaata atttggaaaa acaaacttaa 420
atatgtttag tggttttttt gctcaactgtt caagaataat ctcgtttat cctacttgaa 480
ctagaagttt atatacataa acacgtgaat atttaaacga ccgtacataa acacatgtat 540
cgatcaaata caaatttata tgagactaga atccaagatg aggatgactc tagcagaata 600
tacacagcta agaatttgta caagagatc gaaaaataga ttctaatcat ttaaaaaaaga 660
tatggatttc agttacggat tgatattacc attacgcagt agtacatata cataattttt 720
tgggtttttt ttaccgataa tagaatggaa atgttggttt aaaaatattt gttttactaa 780
aactcgaaaa atgttaacta tataatgtct ttccgcattttt aaattgaaac aaaactgtaa 840
tacaaattat gttaagccat tgcaattttt aaatccacgg gtagttaatc ctcagaagat 900
tatgttaagt ctacaaattt tctctttttaga ttagtaaggat ttgagacaaa attatgtata 960
ccttgcaggg gtataaagggt cactgcatttgcattt tcagacttcattt catgaagcca aagagtcgtc 1020
tctgtcctaa agatatctac agctgctcg cctgttgcattt gagaagaaat tgaatgtata 1080
gagatcccattt ctagcgtttc acgtttgcgt tctccgtcgc aactttggcg gttgttgact 1140
ttttttctta tggcgtttttt tgactaattt tcttcaggatg agagtgtata caagaaaactt 1200
aatattcgaa aagaaagaaa aaaaaggcaa gaaaactattt gtcgaaaaga cataaatgac 1260
actaaaattt gatttataa aatggtatattt atgtttgggtt gaatttataa tcattaccaa 1320

aatcaaaggaa aggagagagg gacctcttcg tgcttatgtat ttccctccta aacaactgct 1380
cccactatcc tttttactt ccaacaaaat cattcacacg agaaaatctg tctcgatc 1440.
actttcatgc aaaattaaac taaatttgg tatttttgt caagttcttg ctgtttaag 1500
tgcatttattt ggtaatacta tatgtgtgga tatacacatc caagctaatac aataattgat 1560
ctccctctgc ttatcaataa attacaccac attagctaattt caagctaata aattacacca 1620
cattctctta tcaatttttata tatggtataaa ataaaacaac cgactatagg ctacagagtt 1680
ggtattaagg cattattgcc ttcttagtgcg aggaattttt ttgttatgtat aacactcg 1740
ggaaaaaaat ccagcctaattt atgctcattt aaaggataat tgatttaat gcttaatca 1800
ttaaaaataaa aggttttgc tttaaagggt taccaccgct taattcatca ttaggagaat 1860
attaactttt atcgaattt caaaataactt tttaaacaca taagaaaattt ttcagcattt 1920
ttaaaaataaag ggtacatttta ttgggttcaa taaatatgtt tccacgtaaa gtttggaggt 1980
ttaaccacat gaatgtttt tgatttaaaa aacacataaa ttgttagtta attacacatt 2040
ttaaccgtc catccagattt gtaataagt gacaatctga aaacattttt tttttcttg 2100
aatcttgcattt aaattctctc tgctgcatac ttgcaggcat ttgaccaacg actatacata 2160
ttgaaagcaa aatatccacc agggatgata gggtagatc ccacattcaa tatctttgt 2220
ctttgttattt tatggaaaac aaatattttt cagaaaaaaa acgtttcttc tctagtggt 2280
taagtataag ataataacaa aatttaatac tttagttaatg tatttactat cttcaaaactt 2340
accatccctt aacatataa ttgatcaattt ttatTTTTT ttactaaactt acttccacta 2400
aaaaaatgca aaagaagaga tatatattt agtcaaagta ataaaagatg gatgggtgat 2460
tcttcagcaa aacggcgccg tagaggtgtc ttatcctaca ttacagctgg gttgtggcag 2520
acatcatagg gcctacgtat atttgagctt tactgtacgt aaagctttaa catatctgt 2580
tagttctcac tgtacaaaca aaacaaaatc caattcgtaa catatataca aataactacta 2640
gtactagattt acgctacgtt tacatcgctt ttgcgcaaat ttctaaacta atctatacaa 2700
caaacttcaa tgttttttt gtaatttata tttaacccaa gtttgaattt gtgcatttggg 2760
agctacactc tagtccccctt ttcccccacaa aataatctcc ttacatcgac cggtaaagt 2820
attaaacca acaaattttt atttgttgcgtaa gaaggtacaa acatgtcaca tatatagaga 2880
cagcatcggtt tatacaaata atgttcgatg ttattggaaa tcaaataataa atacgaatta 2940
gcgactcaact tggtttataa gtttggaaaga taatgaaata aaaaatgaat tcaaaggata 3000
cagagctata tatgtcggtt catttagagc cgtgaccacaa agtttgcgtg taatttctac 3060
ggtcggcat aagaaattttt ggacttttct tcaccctttt atgaacttct gtatagttt 3120
tgtcggattt tatatttgc ttctgtatattttt gtttttttctt aataatgata cgtaaattca 3180
cgataagaaa gacttctttt tatttaattt gattttaaaac ttttgcgtt gggaaatgact 3240
catacacaag gttaaagttt gatggtatcc aatttacaaa aatgtttcga gagtgcgttc 3300
gagtgtccta ccaccatcgta accaactcgatg atgggtttat tatttagttt ttttcttctt 3360
tttccaatgt cttaataattt gaaccactctt aaatttctttt tttaaatttta ggttaagaat 3420
cttgaattttt ctgttgattt taaaccaagg tttaaatttcaattt ttcttagcac aaaaaaaaaa 3480
aaaaggtttt caatttataa agaatctaaa ttttttgagt tcaagagttt aatgatagct 3540
gaaaagttt gaatgattgc aagtttgcac cagaatggc gatgttagtac atatcaaaaa 3600
catgcatcaa aataaatattt cgtgcttagc aagagaaaacg attgaataa acagaacaat 3660
cgtaaccac tttaaaaatct tagaataattt ttgttagtgc aattttctgtt aagagagagg 3720
tatcatatct tacaaaaaaa aactcatatc agataaaaata atgttgcac atcgatcc 3780
agatgtttt tgctgtcatc agttgtatttgc taactcgatc tttagccata tagttctaag 3840
ttttaaatgtt ttcaaaagac ttacaaaaaa taaaataataa ataaaggttgcgatggg 3900
ctaaaagcga aaaataaaaaa taaaataaaa gtaaagaaaac gtctttctca ataagaacac 3960
agatcccaac ggattcaaac agcaatatttgc tgctttgcgc ttctcttta ttataatatc 4020
ctctcaaaaaa ccctctccta tattcctccta aagccccccct tccttgcgtc tctaccgcaa 4080
caaagaaaaaa acaaaaagttt gagaaaaaatg gtgtgttgcgt tttgttaacca atgattgggt 4140
tttagcttac tacttcgaga gattataaga aagaaaagagt gaagatacat tatagaaaga 4200
agagaagcag aaaccaaaaaa aagaaacc 4228

```

<210> 4
<211> 1738
<212> DNA
<213> Brassica napus

<220>
<223> canola AINTEGUMENTA (ANT) partial cDNA including
coding region

```

<220>
<221> CDS
<222> (1)..(1647)
<223> canola AINTEGUMANTA (A

<400> 4
 atg aag tct ttt tgt gat aat gat gat agt aat acg act aat ttg cta 48
 Met Lys Ser Phe Cys Asp Asn Asp Asp Ser Asn Thr Thr Asn Leu Leu
 1 5 10 15

 ggg ttc tcg ttg tct tca aat atg ttg aaa atg ggt ggt gga gaa gct 96
 Gly Phe Ser Leu Ser Ser Asn Met Leu Lys Met Gly Gly Gly Glu Ala
 20 25 30

 ctt tac tca tct tcg tcg tct tca gtt gca act tct tct gtt cca cca 144
 Leu Tyr Ser Ser Ser Ser Val Ala Thr Ser Ser Val Pro Pro
 35 40 45

 cag ctt gtt gtt ggc gac aac agt agc aac tat gga gtt tgc tac ggt 192
 Gln Leu Val Val Gly Asp Asn Ser Ser Asn Tyr Gly Val Cys Tyr Gly
 50 55 60

 tct aac tta gca gct agg gaa atg tat tct caa atg tct gtg atg ccc 240
 Ser Asn Leu Ala Ala Arg Glu Met Tyr Ser Gln Met Ser Val Met Pro
 65 70 75 80

 ctc aga tct gac ggt tct ctt tgc tta atg gaa gct ctc aac aga tct 288
 Leu Arg Ser Asp Gly Ser Leu Cys Leu Met Glu Ala Leu Asn Arg Ser
 85 90 95

 tct cac tcg aat aat cat cac cat agt caa gtt tca tct cca aag atg 336
 Ser His Ser Asn Asn His His Ser Gln Val Ser Ser Pro Lys Met
 100 105 110

 gaa gat ttc ttt ggg acc cat cat cac aac aca agt cac aaa gaa gcc 384
 Glu Asp Phe Phe Gly Thr His His His Asn Thr Ser His Lys Glu Ala
 115 120 125

 atg gat ctt agc tta gat agt tta ttc tac aat acc act cat gcg cca 432
 Met Asp Leu Ser Leu Asp Ser Leu Phe Tyr Asn Thr Thr His Ala Pro
 130 135 140

 aac aac aac acc aac ttt caa gag ttc ttt agc ttc cct caa act aga 480
 Asn Asn Asn Thr Asn Phe Gln Glu Phe Phe Ser Phe Pro Gln Thr Arg
 145 150 155 160

 aac cac cat gag gaa gaa aca aga aac tac gag aat gac cct ggt ttg 528
 Asn His His Glu Glu Thr Arg Asn Tyr Glu Asn Asp Pro Gly Leu
 165 170 175

 aca cat gga gga ggg tct ttt aat gta ggg gta tat ggg gaa ttt caa 576
 Thr His Gly Gly Ser Phe Asn Val Gly Val Tyr Gly Glu Phe Gln
 180 185 190

 cag tca ctg agc ttg tcc atg agc cct ggg tca caa tct agc tgc atc 624
 Gln Ser Leu Ser Leu Ser Met Ser Pro Gly Ser Gln Ser Ser Cys Ile
 195 200 205

 act gcc tct cat cac cac caa aac caa act caa aac cac cag cag atc 672
 Thr Ala Ser His His Gln Asn Gln Thr Gln Asn His Gln Gln Ile
 210 215 220

tct gaa gct ttg gtc gag aca agt gct gga ttt gag aca aca aca atg Ser Glu Ala Leu Val Glu Thr Ser Ala Gly Phe Glu Thr Thr Thr Met 225	230	235	240	720
gcg gct gct gca aag aag aag aga gga caa gaa gtt gtc gtt gga Ala Ala Ala Ala Lys Lys Arg Gly Gln Glu Val Val Val Gly 245	250		255	768
cag aaa cag att gtt cat aga aaa tct att gat act ttt gga caa cga Gln Lys Gln Ile Val His Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg 260	265		270	816
act tcg caa tac cga ggc gtt aca aga cat aga tgg act ggt agg tat Thr Ser Gln Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr 275	280		285	864
gaa gct cat cta tgg gac aat agt ttc aag aag gaa ggt cat agc aga Glu Ala His Leu Trp Asp Asn Ser Phe Lys Lys Glu Gly His Ser Arg 290	295		300	912
aaa gga aga caa gtt tat ctg ggg ggt tat gat atg gag gag aaa gct Lys Gly Arg Gln Val Tyr Leu Gly Tyr Asp Met Glu Glu Lys Ala 305	310		315	320
gct cga gca tat gat ctt gct gca ctc aag tac tgg ggt ccc tct act Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Ser Thr 325	330		335	1008
cac act aat ttc tct gtg gag aat tat cag aaa gag att gat gac atg His Thr Asn Phe Ser Val Glu Asn Tyr Gln Lys Glu Ile Asp Asp Met 340	345		350	1056
aag aac atg act cga caa gaa tat gtt gct cac ttg aga aga aaa acc Lys Asn Met Thr Arg Gln Glu Tyr Val Ala His Leu Arg Arg Lys Thr 355	360		365	1104
agt ggt ttc tct agg ggt gct tcc atc tat aga gga gtc acc aga cat Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His 370	375		380	1152
cac cag cat gga agg tgg caa gct cggt atc ggt aga gtc gct gga aac His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn 385	390		395	400
aaa gat ctc tac ctt gga act ttc gga act caa gaa gaa gcg gcg gaa Lys Asp Leu Tyr Leu Gly Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu 405	410		415	1248
gcc tat gat gta gca gct atc aag ttc cgt ggc aca aac gcg gtg act Ala Tyr Asp Val Ala Ala Ile Lys Phe Arg Gly Thr Asn Ala Val Thr 420	425		430	1296
aac ttt gac ata aca agg tac gat gtt gat cgc ata atg gct agt aac Asn Phe Asp Ile Thr Arg Tyr Asp Val Asp Arg Ile Met Ala Ser Asn 435	440		445	1344
act ctc ttg tct gga gag atg gct cga agg aac agc aac agc atc gtg Thr Leu Leu Ser Gly Glu Met Ala Arg Arg Asn Ser Asn Ser Ile Val 450	455		460	1392

gtc cgc aac att agc gac gag gaa gcc gct tta acc gct gtc gtg aac		1440
Val Arg Asn Ile Ser Asp Glu Glu Ala Ala Leu Thr Ala Val Val Asn		
465	470	475
		480
ggt ggt tcc aat aag gaa gtg ggt agc ccg gag agg gtt ttg agt ttt		1488
Gly Gly Ser Asn Lys Glu Val Gly Ser Pro Glu Arg Val Leu Ser Phe		
485	490	495
ccg acg ata ttt gcg ttg cct caa gtt ggt ccg aag atg ttc gga gca		1536
Pro Thr Ile Phe Ala Leu Pro Gln Val Gly Pro Lys Met Phe Gly Ala		
500	505	510
aat gtg gtc gga aat atg agt tct tgg act acg aac cct aat gct gat		1584
Asn Val Val Gly Asn Met Ser Ser Trp Thr Thr Asn Pro Asn Ala Asp		
515	520	525
ctc aag acc gtt tct ctt act ctg ccg cag atg ccg gtt ttc gct gcg		1632
Leu Lys Thr Val Ser Leu Thr Leu Pro Gln Met Pro Val Phe Ala Ala		
530	535	540
tgg gct gat tct taa ttcaatctaa tggcttaactc tggttttctt ggtttagggt		1687
Trp Ala Asp Ser		
545		
ccaagtgttt aagtttatct ccgggttat ccggtttgaa ctacaattcg g		1738

<210> 5
 <211> 548
 <212> PRT
 <213> Brassica napus
 <223> canola AINTEGUMENTA (ANT)

<400> 5			
Met Lys Ser Phe Cys Asp Asn Asp Asp Ser Asn Thr Thr Asn Leu Leu			
1	5	10	15
Gly Phe Ser Leu Ser Ser Asn Met Leu Lys Met Gly Gly Gly Glu Ala			
20	25	30	
Leu Tyr Ser Ser Ser Ser Val Ala Thr Ser Ser Val Pro Pro			
35	40	45	
Gln Leu Val Val Gly Asp Asn Ser Ser Asn Tyr Gly Val Cys Tyr Gly			
50	55	60	
Ser Asn Leu Ala Ala Arg Glu Met Tyr Ser Gln Met Ser Val Met Pro			
65	70	75	80
Leu Arg Ser Asp Gly Ser Leu Cys Leu Met Glu Ala Leu Asn Arg Ser			
85	90	95	
Ser His Ser Asn Asn His His Ser Gln Val Ser Ser Pro Lys Met			
100	105	110	
Glu Asp Phe Phe Gly Thr His His Asn Thr Ser His Lys Glu Ala			
115	120	125	
Met Asp Leu Ser Leu Asp Ser Leu Phe Tyr Asn Thr Thr His Ala Pro			
130	135	140	
Asn Asn Asn Thr Asn Phe Gln Glu Phe Phe Ser Phe Pro Gln Thr Arg			
145	150	155	160
Asn His His Glu Glu Glu Thr Arg Asn Tyr Glu Asn Asp Pro Gly Leu			
165	170	175	
Thr His Gly Gly Ser Phe Asn Val Gly Val Tyr Gly Glu Phe Gln			
180	185	190	
Gln Ser Leu Ser Leu Ser Met Ser Pro Gly Ser Gln Ser Ser Cys Ile			
195	200	205	

Thr Ala Ser His His Gln Asn Gln Thr Gln Asn His Gln Gln Ile
 210 215 220
 Ser Glu Ala Leu Val Glu Thr Ser Ala Gly Phe Glu Thr Thr Thr Met
 225 230 235 240
 Ala Ala Ala Ala Lys Lys Lys Arg Gly Gln Glu Val Val Val Gly
 245 250 255
 Gln Lys Gln Ile Val His Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg
 260 265 270
 Thr Ser Gln Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr
 275 280 285
 Glu Ala His Leu Trp Asp Asn Ser Phe Lys Lys Glu Gly His Ser Arg
 290 295 300
 Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Met Glu Glu Lys Ala
 305 310 315 320
 Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Ser Thr
 325 330 335
 His Thr Asn Phe Ser Val Glu Asn Tyr Gln Lys Glu Ile Asp Asp Met
 340 345 350
 Lys Asn Met Thr Arg Gln Glu Tyr Val Ala His Leu Arg Arg Lys Thr
 355 360 365
 Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His
 370 375 380
 His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn
 385 390 395 400
 Lys Asp Leu Tyr Leu Gly Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu
 405 410 415
 Ala Tyr Asp Val Ala Ala Ile Lys Phe Arg Gly Thr Asn Ala Val Thr
 420 425 430
 Asn Phe Asp Ile Thr Arg Tyr Asp Val Asp Arg Ile Met Ala Ser Asn
 435 440 445
 Thr Leu Leu Ser Gly Glu Met Ala Arg Arg Asn Ser Asn Ser Ile Val
 450 455 460
 Val Arg Asn Ile Ser Asp Glu Glu Ala Ala Leu Thr Ala Val Val Asn
 465 470 475 480
 Gly Gly Ser Asn Lys Glu Val Gly Ser Pro Glu Arg Val Leu Ser Phe
 485 490 495
 Pro Thr Ile Phe Ala Leu Pro Gln Val Gly Pro Lys Met Phe Gly Ala
 500 505 510
 Asn Val Val Gly Asn Met Ser Ser Trp Thr Thr Asn Pro Asn Ala Asp
 515 520 525
 Leu Lys Thr Val Ser Leu Thr Leu Pro Gln Met Pro Val Phe Ala Ala
 530 535 540
 Trp Ala Asp Ser
 545

<210> 6
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:consensus ANT
 polynucleotide sequence-1

<400> 6
 atgaagtctt tttgtgataa tgatgatagt aat

<210> 7
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus ANT
polynucleotide sequence-2

<400> 7
acgactaatt tggtagggtt ctcattgtct tcaaataatg

39

<210> 8
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus ANT
polynucleotide sequence-3

<400> 8
agaatcagcc caagcagcga aaaccggcat ctgcggca

38